

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
10 May 2001 (10.05.2001)

PCT

(10) International Publication Number
WO 01/32710 A1

(51) International Patent Classification: C07K 14/72,
C07H 21/04, C12N 15/00, 15/63, 15/85, 15/86, G01N
33/53

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(21) International Application Number: PCT/US00/29426

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(22) International Filing Date: 25 October 2000 (25.10.2000)

(25) Filing Language: English

(81) Designated States (*national*): CA, JP, US.

(26) Publication Language: English

(84) Designated States (*regional*): European patent (AT, BE,
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC,
NL, PT, SE).

(30) Priority Data:
60/162,264 29 October 1999 (29.10.1999) US

Published:
— With international search report.

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*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

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(54) Title: DOG AND RABBIT MOTILIN RECEPTOR ORTHOLOGS

(57) Abstract: The present invention features polypeptides and nucleic acids related to the dog and rabbit motilin receptor, and uses of such polypeptides and nucleic acids. The dog motilin receptor exon 1 amino acid sequence is provided for by SEQ. ID. NO. 1, the rabbit motilin receptor amino acid sequence is provided for by SEQ. ID. NO. 2, the nucleic acid sequence encoding for exon 1 of the dog motilin receptor is provided for by SEQ. ID. NO. 3, and the nucleic acid sequence encoding for the rabbit motilin receptor is provided for by SEQ. ID. NO. 4.



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TITLE OF THE INVENTION

DOG AND RABBIT MOTILIN RECEPTOR ORTHOLOGS

CROSS-REFERENCE TO RELATED APPLICATIONS

5 The present application claims priority to U.S. Serial No. 60/162,264, filed October 29, 1999, hereby incorporated by reference herein.

BACKGROUND OF THE INVENTION

10 The references cited herein are not admitted to be prior art to the claimed invention.

 Motilin is a 22 amino acid peptide hormone affecting gastric motility. Motilin has been found to induce smooth muscle contractions in the gastrointestinal tract of different species including humans, cats, rabbits, dogs, and chickens. (Peeters and Depoortere, *Digestive Diseases and Sciences* 39:765-785, 1994; Van Assche, *et al.*, *European Journal of Pharmacology* 337:267-274, 1997; Depoortere and Peters, *American Journal of Physiology* 272:G994 (1997); Kitazawa, *et al.*, *Peptides* 16:1243-1252, 1995; and Itoh, *Peptides* 18:593-608, 1997.)

 The effects of motilin include inducing interdigestive (phase III) antrum and duodenal contractions. (Itoh, *Peptides* 18:593-608, 1997; Poitras, in *Gut Peptides: Biochemistry and Physiology*, J. H. Walsh and G. J. Dockray, Eds. (Raven, New York, 1994), pp. 261-304; and Tonini, *Pharmacol. Res.* 33:217-226, 1996.) The antibiotic erythromycin induces similar effects that may be mediated by motilin receptors. (Itoh, *et al.*, *American Journal of Physiology* 247:G688-G694, 1984; and Weber, *et al.*, *American Journal of Gastroenterology* 88:485-490, 1993.) Erythromycin produces side effects including vomiting, nausea, diarrhea and abdominal discomfort. (Tonini, *Pharmacol. Res.* 33:217-226, 1996.)

SUMMARY OF THE INVENTION

30 The present invention features polypeptides and nucleic acids related to the dog and rabbit motilin receptor, and uses of such polypeptides and nucleic acids. The dog motilin receptor exon 1 amino acid sequence is provided for by SEQ. ID. NO. 1, the rabbit motilin receptor amino acid sequence is provided for by SEQ. ID. NO. 2, the nucleic acid sequence encoding for exon 1 of the dog motilin receptor is provided for by SEQ. ID. NO. 3,

and the nucleic acid sequence encoding for the rabbit motilin receptor is provided for by SEQ. ID. NO. 4.

Polypeptides related to the dog or rabbit motilin receptor contain a region of at least 9 contiguous amino acids that are present in the dog or rabbit motilin receptor. Such polypeptides may contain additional regions including regions present, or not present, in the dog or rabbit motilin receptor.

Nucleic acids related to the dog or rabbit motilin receptor contain a region of at least 18 contiguous nucleotides that is present in the dog or rabbit motilin receptor nucleic acid or the complement thereof. Such nucleic acids may contain additional regions including regions present, or not present, in the dog or rabbit motilin receptor nucleic acid.

Thus, a first aspect of the present invention describes a purified polypeptide comprising a unique amino acid region of a dog or rabbit motilin receptor. The unique region is at least 9 amino acids in length.

A "unique amino acid region" is a region of contiguous amino acids present in SEQ. ID. NOs. 1 or 2 that is not present in SEQ. ID. NOs. 5 or 6. SEQ. ID. NO. 5 is a human motilin receptor amino acid sequence and SEQ. ID. NO. 6 is an amino acid sequence for *Spheroides nephelus* 75E7. The unique region may contain segments of contiguous amino acids present in SEQ. ID. NOs. 5 or 6 smaller than the indicated unique region size.

A "purified polypeptide" represents at least 10% of the total protein present in a sample or preparation. In preferred embodiments, the purified polypeptide represents at least about 50%, at least about 75%, or at least about 95% of the total protein in a sample or preparation. Reference to "purified polypeptide" does not require that the polypeptide has undergone any purification and may include, for example, chemically synthesized polypeptide that has not been purified.

Another aspect of the present invention describes a purified nucleic acid comprising a nucleotide sequence encoding for a unique amino acid region from the dog or rabbit motilin receptor or the complement thereof. The encoded for region is at least 9 amino acids in length.

A "purified nucleic acid" represents at least 10% of the total nucleic acid present in a sample or preparation. In preferred embodiments, the purified nucleic acid represents at least about 50%, at least about 75%, or at least about 95% of the total nucleic acid a sample or preparation. Reference to "purified nucleic acid" does not require that the nucleic acid has undergone any purification and may include, for example, chemically synthesized nucleic acid that has not been purified.

Another aspect of the present invention describes a purified nucleic acid comprising a unique nucleotide sequence region of a dog or rabbit motilin receptor nucleic acid sequence. The unique nucleotide sequence region is at least 18 nucleotides in length.

5 A "unique nucleotide sequence region" is a region that comprises at least 18 contiguous nucleotides of SEQ. ID. NOs. 3 or 4 that is not present in SEQ. ID. NOs. 7 or 8. SEQ. ID. NO. 7 is the nucleotide sequence encoding for a human motilin receptor and SEQ. ID. NO. 8 is the nucleotide sequence encoding for *Spheroides nephelus* 75E7. The unique region may contain segments of contiguous nucleotides present in SEQ. ID. NOs. 7 or 8 smaller than the indicated unique region size.

10 Another aspect of the present invention describes an expression vector. The expression vector comprises a recombinant nucleotide sequence encoding for a unique amino acid region of a dog or rabbit motilin receptor.

15 A "recombinant nucleotide sequence" is a sequence that is present on a nucleic acid containing one or more nucleic acid regions not naturally associated with that sequence. Examples of such regions that may be present include one or more regulatory elements not naturally associated with the sequence, viral elements, and selectable markers.

Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a unique amino acid region of a dog or rabbit motilin receptor. The expression vector contains a promoter that is functionally coupled to
20 nucleic acid encoding for the unique region and is recognized by an RNA polymerase present in the cell.

Another aspect of the present invention describes a recombinant cell made by introducing an expression vector encoding for a unique amino acid region of a dog or rabbit motilin receptor into a cell. The expression vector can be used to insert the dog or rabbit
25 nucleic acid into the genome of the host, or can exist as an autonomous piece of nucleic acid.

Another aspect of the present invention describes a method of measuring the ability of a compound to effect motilin receptor activity. The method involves providing the compound to a recombinant cell expressing a functional motilin receptor containing a unique dog or rabbit amino acid region from a recombinant nucleic acid and measuring motilin
30 receptor activity. Preferably, the recombinant nucleic acid is present on an expression vector.

Another aspect of the present invention describes a method of producing a motilin receptor polypeptide. The method involves the step of growing a recombinant cell able to express a dog or rabbit motilin receptor polypeptide under conditions wherein the polypeptide is expressed from an expression vector.

Other features and advantages of the present invention are apparent from the additional descriptions provided herein including the different examples. The provided examples illustrate different components and methodology useful in practicing the present invention. The examples do not limit the claimed invention. Based on the present disclosure
5 the skilled artisan can identify and employ other components and methodology useful for practicing the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 illustrates a comparison of the protein sequence for the dog motilin
10 receptor exon 1 (SEQ. ID. NO. 1), the rabbit motilin receptor (SEQ. ID. NO. 2), the human motilin receptor (SEQ. ID. NO. 5) and *Spheroides nephelus* 75E7 (SEQ. ID. NO. 6).

Figures 2A-2C illustrate a comparison of the DNA sequence encoding for the dog motilin receptor exon 1 (SEQ. ID. NO. 3), the rabbit motilin receptor (SEQ. ID. NO. 4), the human motilin receptor (SEQ. ID. NO. 7) and *Spheroides nephelus* 75E7 (SEQ. ID. NO.
15 8).

DETAILED DESCRIPTION OF THE INVENTION

The present invention features polypeptides and nucleic acids related to the dog and rabbit motilin receptor. Preferred polypeptides contain an amino acid region not
20 present in the human motilin receptor or *Spheroides nephelus* 75E7. Preferred nucleic acids contain a nucleotide region not present in nucleic acid encoding for the human motilin receptor or *Spheroides nephelus* 75E7.

The amino acid sequence and encoding DNA sequence for two alternatively spliced forms of the human motilin receptor (MTL-R1 and MTL-R2) are described by
25 Feighner, *et al.*, *Science* 284:2184-2188, 1999 (not admitted to be prior art to the claimed invention). Additionally, an amino acid sequence for genomic DNA encoding for "GPR38" is described by McKee, *et al.*, *Genomics* 46:426-434, 1997. Feighner, *et al.*, identifies GPR38 as the motilin receptor and indicates the presence of an intron.

The *Spheroides nephelus* gene 75E7 has a high level of homology to the
30 human motilin receptor. The protein sequence of 75E7 is 54% identical to human motilin receptor (MTL-R1) and contains a similar exon-intron structure. (Feighner, *et al.*, *Science* 284:2184-2188, 1999.)

A preferred use of dog and rabbit motilin receptor polypeptides and nucleic acids is in an *in vitro* functional assay that measures whether a compound acts differently at

the dog or rabbit receptor than at the human receptor. Such an assay can be used to help evaluate whether a dog or rabbit model provides a useful test system in looking for a human therapeutic compound.

Therapeutic uses of compounds active at the motilin receptor include the treatment gastrointestinal diseases and disorders such as gastric motility disorders (intrinsic myopathies or neuropathy), gastroparesis, irritable bowel syndrome, and diarrhea. Additionally, compounds active at the motilin receptor can be used as a research tool for studying motilin receptor activity.

MOTILIN RECEPTOR RELATED POLYPEPTIDES

Polypeptides related to the dog and rabbit polypeptide contain a unique dog or rabbit amino acid region. In addition to the unique amino acid region, regions that may, or may not, be related to the dog or rabbit motilin receptor polypeptide may be present in the polypeptides. Such polypeptides have a variety of uses, such as providing a component of a functional motilin receptor; being used as an immunogen to produce antibodies binding to the dog or rabbit motilin receptor; being used as a target to identify compounds binding to the motilin receptor; and/or being used in assays to measure the ability of a compound to effect motilin receptor activity.

Unique dog and rabbit amino acid regions can readily be identified based on a comparison of the dog and rabbit motilin receptor sequences described herein, with the human motilin receptor and the *Spheroides nephelus* 75E7 protein sequences. Such a sequence comparison is illustrated in Figure 1. Examples of unique dog amino acid regions include the following: GPGNSSDGA (SEQ. ID. NO. 9); VCLGLFAVGV (SEQ. ID. NO. 10); ALLSSRRRA (SEQ. ID. NO. 11); APFFFLVGVEQDAGG (SEQ. ID. NO. 12); and CLCVLYGRI (SEQ. ID. NO. 13). Examples of unique rabbit amino acid regions include the following: DPAVFAAPDR (SEQ. ID. NO. 14); NGTVPLDPS (SEQ. ID. NO. 15); SPAPASPPSGPG (SEQ. ID. NO. 16); RRLRESRAG (SEQ. ID. NO. 17); and SGVCGSRGPEQD (SEQ. ID. NO. 18).

The definition of unique amino acid region is with respect to human motilin receptor and *Spheroides nephelus* 75E7 protein sequences. Thus, a unique amino acid region may be present in a motilin receptor sequence from one or more species other than the human motilin receptor or *Spheroides nephelus* 75E7 protein sequence, or in a non-motilin receptor sequence. For example, SEQ. ID. NO. 10 is present in both the dog and rabbit motilin receptor.

In different embodiments a dog or rabbit motilin receptor related polypeptide comprises or consists of a unique amino acid region at least 18, at least 27, or at least 54, bases in length. Preferably, the dog or rabbit motilin receptor related polypeptide comprises or consists of the amino acid sequence of SEQ. ID. NO. 1 or SEQ. ID. NO. 2.

5 Polypeptides can be produced using standard techniques including those involving chemical synthesis and those involving biochemical synthesis. Techniques for chemical synthesis of polypeptides are well known in the art. (See *e.g.*, Vincent, in *Peptide and Protein Drug Delivery*, New York, N.Y., Dekker, 1990.)

Biochemical synthesis techniques for polypeptides are also well known in the
10 art. Such techniques employ a nucleic acid template for polypeptide synthesis. The genetic code providing the sequences of nucleic acid triplets coding for particular amino acids is well known in the art. (See, *e.g.*, Lewin *GENES IV*, p. 119, Oxford University Press, 1990.) Examples of techniques for introducing nucleic acid into a cell and expressing the nucleic acid to produce protein are provided in references such as Ausubel, *Current Protocols in*
15 *Molecular Biology*, John Wiley, 1987-1998, and Sambrook, *et al.*, in *Molecular Cloning, A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989.

Functional Motilin Receptor Derivatives

Functional motilin receptors can bind motilin and transduce an intracellular
20 signal. Functional motilin receptors include the dog and rabbit motilin receptors, and receptors having motilin receptor activity that contain a unique dog or rabbit amino acid region as a component.

Starting with a motilin receptor obtained from a particular source, derivatives can be produced having motilin receptor activity. Such derivatives include polypeptides with
25 amino acid substitutions, additional and deletions. Changes made to produce functional derivatives should be made outside of the motilin-binding domain and in a manner not altering the tertiary structure. The ability of a polypeptide to have motilin receptor activity can be confirmed using techniques such as those measuring G-protein activity.

The sequence comparison provided in Figure 1 illustrates amino acids that
30 vary between the human, dog, and rabbit motilin receptors. Such variable amino acids are good targets for alterations.

Additionally, amino acids are classified into certain types based on the structure of their R-groups. Substituting different amino acids within a particular group, such

as substituting valine for leucine, arginine for lysine, and asparagine for glutamine may not cause a change in functionality of the polypeptide.

Motilin Antibodies

5 Antibodies recognizing a dog or rabbit motilin receptor polypeptide can be produced using a polypeptide of SEQ. ID. NO. 1, SEQ. ID. NO. 2, or a fragment thereof as an immunogen. Fragments should be at least 9 amino acids in length and preferably consist of a unique amino acid region.

10 Antibodies to the motilin receptor have different uses such as being used to identify the presence of motilin receptor polypeptides and for isolating motilin receptor polypeptides. Examples of techniques for producing and using antibodies are described in Ausubel, *Current Protocols in Molecular Biology*, John Wiley, 1987-1998, Harlow, *et al.*, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, and Kohler, *et al.*, *Nature* 256:495-497, 1975.

Binding Assays

15 Assays measuring the ability of a compound to bind the dog or motilin receptor can be performed using a polypeptide of SEQ. ID. NO. 1, SEQ. ID. NO. 2, or a fragment thereof as a target. Fragments should be at least 9 amino acids in length and
20 contain a site to which either an agonist, antagonist, or allosteric modulator binds. Different types of assay formats can be employed including competitive and non-competitive assays.

 Compounds identified as binding to a full-length receptor or a receptor fragment can be used to determine the locus of a binding site by testing out the ability of the compound to bind to smaller length fragments. For example, motilin binds to the motilin
25 receptor and labeled motilin can be used to identify that portion of the receptor to which motilin binds. Fragments identified as containing a compound binding site can be used to test for additional compounds that bind to the binding site.

 Preferred polypeptide fragments used in a binding assay consist of a unique amino acid region. However, fragments containing additional amino acid sequences can be
30 employed, for example, to facilitate attachment to a column.

 Binding assays can be performed using individual compounds or preparations containing different compounds. A preparation containing different compounds wherein one or more compounds bind to the motilin receptor can be divided into smaller groups to

identify compound(s) binding to the motilin receptor. In an embodiment of the present invention a test preparation containing at least 10 compounds is used in a binding assay.

Binding assays can be performed using recombinantly produced motilin receptor polypeptides present in different environments. Such environments include, for example, cell extracts and purified cell extracts containing the motilin receptor polypeptide expressed from recombinant nucleic acid; and the use of a purified motilin receptor polypeptide produced by recombinant means which is introduced into a different environment.

10 Functional Assays

Assays involving functional dog or rabbit motilin receptors can be employed to select for compounds active at the motilin receptor and to evaluate the ability of a compound to effect receptor activity. Motilin receptor activity can be measured using different techniques such as detecting a change in the intracellular conformation of the motilin receptor, measuring G-protein activity, or measuring the level of intracellular messengers.

Recombinantly expressed motilin receptor polypeptides can be used to facilitate determining whether a compound is active at the motilin receptor or another receptor. For example, the motilin receptor can be expressed by an expression vector in a cell line such as HEK 293, COS 7, and CHO not normally expressing the receptor, wherein the same cell line without the expression vector or with an expression vector not encoding for a motilin receptor can act as a control.

Motilin receptors appear to activate the phospholipase C signal transduction pathway. Activity of the phospholipase C signal transduction pathway can be measured using standard techniques such as those measuring intracellular Ca^{2+} . Examples of techniques well known in the art that can be employed to measure Ca^{2+} include the use of dyes such as Fura-2 and the use of Ca^{2+} -bioluminescent sensitive reporter proteins such as aequorin. An example of a cell line employing aequorin to measure G protein activity is HEK293/aeq17. (Button, *et al.*, *Cell Calcium* 14:663-671, 1993, and Feighner, *et al.*, *Science* 284:2184-2188, 1999, both of which are hereby incorporated by reference herein.)

Chimeric receptors containing a motilin binding region functionally coupled to polypeptides from other G protein can also be used to measure motilin receptor activity. Such chimeric receptors preferably contain at least one unique dog or rabbit amino acid region. A chimeric motilin receptor contains an N-terminal extracellular domain; a

transmembrane domain made up of transmembrane regions, extracellular loop domains, and intracellular loop domains; and an intracellular carboxy terminus. Preferred chimerics contain the extracellular domain of a motilin dog or rabbit receptor.

The specificity of G protein coupling is determined by intracellular domain(s).

5 A chimeric motilin receptor can be produced to functionally couple to a particular G protein such as a Gq protein or a Gi protein. Such signal swapping allows for the detection of motilin receptor activity by measuring Gq or Gi activity. Techniques for producing chimeric receptors and measuring G protein coupled responses are provided for in, for example, International Application Number WO 97/05252, and U.S. Patent Number 5,264,565, both of
10 which are hereby incorporated by reference herein.

Functional assays can be performed using individual compounds or preparations containing different compounds. A preparation containing different compounds where one or more compounds affect motilin receptor activity can be divided into smaller groups of compounds to identify the compound(s) affecting motilin receptor activity. In an
15 embodiment of the present invention a test preparation containing at least 10 compounds is used in a functional assay.

Functional assays can be performed using recombinantly produced motilin receptor polypeptides present in different environments. Such environments include, for example, cell extracts, and purified cell extracts, containing the motilin receptor polypeptide
20 expressed from recombinant nucleic acid; and the use of a purified motilin receptor polypeptide produced by recombinant means which is introduced into a different environment.

MOTILIN RECEPTOR RELATED NUCLEIC ACID

25 Nucleic acids related to the dog and rabbit motilin receptor nucleic acid contain a unique dog or rabbit nucleotide sequence region. Such nucleic acids have a variety of uses, such as being used as a hybridization probe or PCR primer to identify the presence of dog or rabbit motilin nucleic acid; being used as a hybridization probe or PCR primer to identify nucleic acid encoding for receptors related to the motilin receptor from different
30 sources; and/or being used for recombinant expression of dog or rabbit motilin receptor polypeptide.

Unique dog and rabbit nucleic acid regions can readily be identified based on a comparison of the dog and rabbit motilin receptor nucleic acid sequences described herein,

with the human motilin receptor and the *Spheroides nephelus* 75E7 nucleic acid sequences. Such a sequence comparison is illustrated in Figure 2.

Examples of unique dog nucleic acid regions include the following:

GGCCCCGGGAACAGCAGCGACGGCGCG (SEQ. ID. NO. 19);
5 GGCCGTGTGCCTGGGCCT (SEQ. ID. NO. 20);
CGCGCGCTGCTGTCCCGG (SEQ. ID. NO. 21);
AGGACGCGGGCGGCCCG (SEQ. ID. NO. 22); and
CCGCGAGCTGCGGAGGCG (SEQ. ID. NO. 23).

Examples of unique rabbit nucleic acid regions include the following:

10 TTCGGCCGGGCCCTTCTTCTTT (SEQ. ID. NO. 24);
GGTCTTCGCGGCCCGGA (SEQ. ID. NO. 25);
CGGTACTGTGCCGCTGGA (SEQ. ID. NO. 26);
GCTTTTCTACCTGAGTGC GTCC (SEQ. ID. NO. 27); and
CGAGCGGGGCCAGTGGTG (SEQ. ID. NO. 28).

15 The guidance provided in the present application can be used to obtain the nucleic acid sequence encoding for the full-length dog motilin receptor, to obtain nucleic acids encoding for motilin receptors from additional sources, and to artificially produce a motilin receptor. Obtaining nucleic acids encoding for a motilin receptor from different sources is facilitated using sets of degenerative probes and primers and by the proper
20 selection of hybridization conditions. Sets of degenerative probes and primers are produced taking into account the degeneracy of the genetic code. Adjusting hybridization conditions is useful for controlling probe or primer specificity to allow for hybridization to nucleic acids having similar sequences.

25 Techniques employed for hybridization detection and PCR cloning are well known in the art. Nucleic acid detection techniques are described, for example, in Sambrook, *et al.*, in *Molecular Cloning, A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989. PCR cloning techniques are described, for example, in White, *Methods in Molecular Cloning*, volume 67, Humana Press, 1997.

30 Motilin receptor probes and primers can be used to screen nucleic acid libraries containing, for example, genomic DNA or cDNA. Such libraries are commercially available, and can be produced using techniques such as those described in Ausubel, *Current Protocols in Molecular Biology*, John Wiley, 1987-1998.

Starting with a particular motilin receptor amino acid sequence and the known degeneracy of the genetic code, a large number of different encoding nucleic acid sequences

can be obtained. The degeneracy of the genetic code arises because almost all amino acids are encoded for by different combinations of nucleotide triplets. The translation of a particular codon into a particular amino acid is well known in the art (*see, e.g., Lewin GENES IV, p. 119, Oxford University Press, 1990*). Amino acids are encoded for by codons as follows:

- A=Ala=Alanine: codons GCA, GCC, GCG, GCU
- C=Cys=Cysteine: codons UGC, UGU
- D=Asp=Aspartic acid: codons GAC, GAU
- E=Glu=Glutamic acid: codons GAA, GAG
- 10 F=Phe=Phenylalanine: codons UUC, UUU
- G=Gly=Glycine: codons GGA, GGC, GGG, GGU
- H=His=Histidine: codons CAC, CAU
- I=Ile=Isoleucine: codons AUA, AUC, AUU
- K=Lys=Lysine: codons AAA, AAG
- 15 L=Leu=Leucine: codons UUA, UUG, CUA, CUC, CUG, CUU
- M=Met=Methionine: codon AUG
- N=Asn=Asparagine: codons AAC, AAU
- P=Pro=Proline: codons CCA, CCC, CCG, CCU
- Q=Gln=Glutamine: codons CAA, CAG
- 20 R=Arg=Arginine: codons AGA, AGG, CGA, CGC, CGG, CGU
- S=Ser=Serine: codons AGC, AGU, UCA, UCC, UCG, UCU
- T=Thr=Threonine: codons ACA, ACC, ACG, ACU
- V=Val=Valine: codons GUA, GUC, GUG, GUU
- W=Trp=Tryptophan: codon UGG
- 25 Y=Tyr=Tyrosine: codons UAC, UAU

In different embodiments dog or rabbit motilin receptor related nucleic acid comprises or consists of a unique nucleic acid region at least 27 or at least 54 bases in length. Preferably, the dog or rabbit motilin receptor related nucleic acid comprises or consists of the nucleic acid sequence of SEQ. ID. NO. 3 or SEQ. ID. NO. 4.

- 30 Nucleic acid having a desired sequence can be synthesized using chemical and biochemical techniques. Examples of chemical techniques are described in Ausubel, *Current Protocols in Molecular Biology*, John Wiley, 1987-1998, and Sambrook, *et al.*, in *Molecular Cloning, A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989.

Biochemical synthesis techniques involve the use of a nucleic acid template

and appropriate enzymes such as DNA and/or RNA polymerases. Examples of such techniques include *in vitro* amplification techniques such as PCR and transcription based amplification, and *in vivo* nucleic acid replication. Examples of suitable techniques are provided by Ausubel, *Current Protocols in Molecular Biology*, John Wiley, 1987-1998, 5 Sambrook, *et al.*, in *Molecular Cloning, A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989, and Kacian, *et al.*, U.S. Patent No. 5,480,784.

Motilin Receptor Probes

Detection probes for the dog or rabbit motilin receptor preferably contain a 10 unique dog or rabbit nucleic acid region, or the complement thereof. Such probes can contain additional nucleic acid that may, or may not, be complementary to dog or rabbit motilin receptor nucleic acid. Preferably, additional nucleic acid that is present has a particular purpose such as providing for increased specificity, being a reporter sequence, or being a capture sequence. However, additional nucleic acid need not have a particular 15 purpose.

Probes for the motilin receptor can specifically hybridize to motilin receptor target nucleic acid under appropriate hybridization conditions (*i.e.*, distinguish target nucleic acid from one or more non-target nucleic acid molecules). A preferred non-target nucleic acid is either nucleic acid encoding for the human motilin receptor or the complement 20 thereof. Hybridization occurs through complementary nucleotide bases present on the probe and motilin receptor nucleic acid. Hybridization conditions determine whether two molecules have sufficiently strong interactions with each other to form a stable hybrid.

Probes are composed of nucleic acids or derivatives thereof such as modified nucleic acid and peptide nucleic acid. Modified nucleic acid includes nucleic acid with one 25 or more altered sugar groups, altered internucleotide linkages, and/or altered nucleotide purine or pyrimidine bases. References describing modified nucleic acid include WO 98/02582, U.S. Patent No. 5,859,221 and U.S. Patent No. 5,852,188, each of which are hereby incorporated by reference herein.

The degree of interaction between two molecules that hybridize together is 30 reflected by the T_m of the produced hybrid. The higher the T_m the stronger the interactions and the more stable the hybrid. T_m is effected by numerous factors well known in the art such as the degree of complementarity, the type of complementary bases present (*e.g.*, A-T hybridization versus G-C hybridization), the structure of the nucleic acid backbones, and

solution components. *E.g.*, Sambrook, *et al.*, in *Molecular Cloning, A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989.

Stable hybrids are formed when the T_m of a hybrid is greater than the temperature employed under a particular set of hybridization assay condition. The degree of specificity of a probe can be varied by adjusting the hybridization stringency conditions. Detecting probe hybridization is facilitated through the use of a detectable label. Examples of detectable labels include luminescent, enzymatic, and radioactive labels.

Examples of stringency conditions are provided in Sambrook, *et al.*, in *Molecular Cloning, A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989. An example of high stringency conditions is as follows: Prehybridization of filters containing DNA is carried out for 2 hours to overnight at 65°C in buffer composed of 6X SSC, 5X Denhardt's solution, and 100 µg/ml denatured salmon sperm DNA. Filters are hybridized for 12 to 48 hours at 65°C in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2X SSC, 0.1% SDS. This is followed by a wash in 0.1X SSC, 0.1% SDS at 50°C for 45 minutes before autoradiography. Other procedures using conditions of high stringency would include, for example, either a hybridization step carried out in 5X SSC, 5X Denhardt's solution, 50% formamide at 42°C for 12 to 48 hours or a washing step carried out in 0.2X SSPE, 0.2% SDS at 65°C for 30 to 60 minutes.

Recombinant Expression

Motilin receptor related polypeptides can be expressed from recombinant nucleic acid in a suitable host or in a test tube using a translation system. Recombinantly expressed motilin receptor polypeptides are preferably used in assays to screen for compounds that bind to the motilin receptor and modulate the activity of the receptor.

Preferably, expression is achieved in a host cell using an expression vector. An expression vector contains recombinant nucleic acid encoding for a desired polypeptide along with regulatory elements for proper transcription and processing. The regulatory elements that may be present include those naturally associated with the recombinant nucleic acid and exogenous regulatory elements not naturally associated with the recombinant nucleic acid. Exogenous regulatory elements such as an exogenous promoter can be useful for expressing recombinant nucleic acid in a particular host.

Generally, the regulatory elements that are present include a transcriptional promoter, a ribosome binding site, a terminator, and an optionally present operator. Another preferred element is a polyadenylation signal providing for processing in eukaryotic cells. Preferably, an expression vector also contains an origin of replication for autonomous
5 replication in a host cell, a selectable marker, a limited number of useful restriction enzyme sites, and a potential for high copy number. Examples of expression vectors are cloning vectors, modified cloning vectors, specifically designed plasmids and viruses.

Expression vectors that can be used to provide suitable levels of polypeptide expression in different hosts are well known in the art. Mammalian expression vectors well
10 known in the art include pcDNA3 (Invitrogen), pMC1neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), EBO-pSV2-neo (ATCC 37593), pBPV-1(8-2) (ATCC 37110), pdBPV-MMTneo(342-12) (ATCC 37224), pRSVgpt (ATCC 37199), pRSVneo (ATCC 37198), pSV2-dhfr (ATCC 37146), pUCTag (ATCC 37460), pCI-neo (Promega) and lambda.ZD35 (ATCC 37565). Bacterial expression vectors well known in the art include pET11a
15 (Novagen), lambda gt11 (Invitrogen), pcDNAII (Invitrogen), and pKK223-3 (Pharmacia). Fungal cell expression vectors well known in the art include pYES2 (Invitrogen), Pichia expression vector (Invitrogen). Insect cell expression vectors well known in the art include Blue Bac III (Invitrogen).

Recombinant host cells may be prokaryotic or eukaryotic. Examples of
20 recombinant host cells include the following: bacteria such as *E. coli*; fungal cells such as yeast; mammalian cells such as human, bovine, porcine, monkey and rodent; and insect cells such as *Drosophila* and silkworm derived cell lines. Commercially available mammalian cell lines include L cells L-M(TK.sup.-) (ATCC CCL 1.3), L cells L-M (ATCC CCL 1.2), 293 (ATCC CRL 1573), Raji (ATCC CCL 86), CV-1 (ATCC CCL 70), COS-1 (ATCC CRL
25 1650), COS-7 (ATCC CRL 1651), CHO-K1 (ATCC CCL 61), 3T3 (ATCC CCL 92), NIH/3T3 (ATCC CRL 1658), HeLa (ATCC CCL 2), C127I (ATCC CRL 1616), BS-C-1 (ATCC CCL 26) and MRC-5 (ATCC CCL 171).

Expression vectors may be introduced into host cells using standard techniques. Examples of such techniques include transformation, transfection, lipofection,
30 protoplast fusion, and electroporation.

Motilin receptor nucleic acid can be expressed in a cell without the use of an expression vector employing, for example, synthetic mRNA or native mRNA. Additionally, mRNA can be translated in various cell-free systems such as wheat germ extracts and

reticulocyte extracts, as well as in cell based systems, such as frog oocytes. Introduction of mRNA into cell based systems can be achieved, for example, by microinjection.

EXAMPLES

5 Examples are provided below to further illustrate different features and advantages of the present invention. The examples also illustrate useful methodology for practicing the invention. These examples do not limit the claimed invention.

Example 1: Cloning of the Rabbit Motilin Receptor

10 A rabbit motilin receptor was identified and cloned from a λ DashII genomic library (Stratagene, La Jolla, CA) by screening with a human MTLR probe (exon I & II, GPR38; McKee, *et al.*, *Genomics* 46:426-434, 1977, hereby incorporated by reference herein). Hybridization was performed using reduced-stringency conditions as described below.

15 1.1×10^6 plaque forming units (pfu) were plated on *E. coli* XLBlue MRA (P2) and transferred to nylon membranes (NEF-978A; NEN, Boston, MA). Duplicate membranes were incubated overnight at 30°C in prehybridization solution (50% formamide, 2X Denhardt's, 5X SSPE, 0.1% SDS, 100 μ g/ml salmon sperm DNA) followed by overnight incubation in hybridization solution (50% formamide, 2X Denhardt's, 5X SSPE, 0.1% SDS, 20 10% dextran sulfate, 100 μ g/ml salmon sperm DNA) with 1×10^6 cpm/ml labeled probe and final wash conditions of 1X SSC at 55°C. A clone was identified after two rounds of screening and sequenced with BIG DYE terminator cycle sequencing Ready Reactions (Perkin Elmer, Foster City, CA) on a 377 ABI Prism cycle sequencer (Perkin Elmer, Foster City, CA).

25 To generate a contiguous open reading frame (ORF) for the rabbit motilin receptor, overlapping PCR was performed on exons I and II. PCR products for exons I and II were produced each containing a small portion of the other exon. The primers for exon I, SEQ. ID. NO. 29 (5' gggcccgaattcgccgccATGGGCAGCCCCTGGAACGGCAGC) and SEQ. ID. NO. 30 (5' GGCCAGAACCACCACCAGCAGGACGCGGACGGTCTG), 30 contained an EcoRI site and a "GCC GCC" Kozac sequence. The primers for exon II, SEQ. ID. NO. 31 (5' GTCCGCGTCCTGCTGGTGGTGGTTCTGGCCTTTATAGTG) and SEQ. ID. NO. 32 (5' agtttagcggccgcCTATGCAGCCGTCTTTGTGTTAGC3'), contained a NotI site. The rabbit motilin ORF was then generated from exon I and II templates and primers SEQ. ID. NO. 29 and SEQ. ID. NO. 32.

An Advantage cDNA PCR kit (Clontech, Palo Alto, CA) was used in the PCR reactions generally following manufacture instructions. Two exceptions were the addition of 5% DMSO to the PCR reactions and PCR cycling as follows: 1) 94°C for 1 minute, 2) 5 cycles of 94°C for 30 seconds, 72°C for 3 minutes, 3) 5 cycles of 94°C for 30 seconds, 70°C for 3 minutes, 4) 20 cycles of 94°C for 30 seconds, 68°C for 3 minutes. The rabbit motilin ORF fragment was digested with EcoRI and NotI, gel-purified, ligated into pcDNA3 vector and transformed into SCS1 *E. coli* (Stratagene, La Jolla, CA).

Example 2: Cloning of the Dog Motilin Receptor Exon 1

10 A dog motilin receptor exon was identified and cloned by screening the canine lambda FixII genomic library (Stratagene, La Jolla, CA) with the human MTLR probe (see Example 1). Using techniques illustrated herein, such as those described in Example 1, the full-length clone can readily be obtained.

Hybridization was performed using reduced-stringency conditions. 1.2×10^6 phage plaques of the once amplified library were plated onto *E. coli* XL1-Blue MRA at 30,000 pfu per 150 mm plate. The phage were transferred onto nylon hybridization transfer membranes (NEN, Boston, MA) in duplicate, denatured, neutralized, washed and probed with random primed (Prime-It II kit, Stratagene, La Jolla, CA) P³²dCTP labeled human MTLR exon I and exon II probes. The membranes were prehybridized (50% formamide, 2X Denhardt's, 5X SSPE, 0.1% SDS, 100 µg/mL salmon sperm DNA) for two hours followed by overnight hybridization (50% formamide, 2X Denhardt's, 5X SSPE, 10% dextran sulfate, 0.1% SDS, 100 µg/mL salmon sperm DNA), shaking in a 32°C incubator with probe at 1×10^6 cpm/mL. The filters were washed in 4X SSC, 0.1% SDS solution at 23°C followed by 2X SSC, 0.1% SDS at 42°C and finally 1X SSC, 0.1% SDS at 55°C.

25 After two rounds of plaque purification seven clones were isolated. Lambda DNA was isolated from the seven clones using a liquid lysate preparation. The indicator strain XL1-Blue MRA was lysed with eluted phage and cell debris spun down. The liquid phage stock was treated with RNaseA at 38 µg/mL, 37°C for 30 minutes and PEG-precipitated (10% PEG8000/1M NaCl in SM buffer) overnight at 4°C. Pelleted phage DNA was proteinase K treated (50 µg/mL, 68°C, 15 minutes). This was followed by phenol/chloroform and chloroform extractions and ethanol precipitation.

30 Lambda DNA was spooled out with a sterile pipet tip, washed with 70% ethanol and resuspended in sterile water. Each DNA was digested with a band of restriction enzymes (BamHI, EcoRI, NotI, PstI, SmaI and XbaI), electrophoresed on 1% Seakem GTG

IX TAE agarose gel, southern blotted and probed with human MTLR exon I and II probes as described above. Hybridizing bands were subcloned and sequenced on ABI 377 automated sequencer using Big Dye terminator premix (Perkin Elmer, Foster City, CA). Sequence information obtained was then analyzed using the Sequencer program. Of these, a 2kB NotI
 5 fragment from lambda DNA 35 contained the largest fragment of dog MTLR encoding exon I, the splice junction, and intronic sequence.

Example 3: Dog and Rabbit Motilin Receptor Sequences

The nucleotide and amino acid sequences for SEQ. ID. NOs. 1, 2, 3, and 4 are
 10 provided as follows:

SEQ. ID. NO. 1

MGGPGNSSDGAEGAQLPCDERLCSPFPLGALVPVTAVCLGLFAVGVSGNLVTVLLIG
 RYRDMRTTTNLYLGSMASVDDLILLGLPLDLYRLWRSRPWVFGQLLCRLSLYLGE
 15 CTYATLLHVTALSVERYLAVCRPLRARALLSRRRARALIAALWAVALLSAAPFFFLV
 GVEQDAGGPGLNGSARLARAPSPPPGPEAALFSRECRSPSQLGALRVMLWVTTAYF
 FLPLCLCVLYGRIGRELRRRRGPLRGRAASGRERGHRQAVRVL

SEQ. ID. NO. 2

MGSPWNGSDGPEDAREPPWAALPPCDERRCSPFPLGTLVPVTAVCLGLFAVGVSGN
 VVTVLLIGRYRDMRTTTNLYLGSMASVDDLILLGLPFDLYRLWRSRPWVFGQLLCRL
 SLYVGEGETYASLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAALWAVALLS
 AGPFFFLVGVEQDPAVFAAPDRNGTVPLDPSSPAPASPPSGPGAEEAALFSRECRPSR
 AQLGLLRVMLWVTTAYFFLPFLCLSILYGLIARQLWRGRGPLRGPAATGRERGHRQT
 25 VRVLLVVVLAFIGVWLPFHVGRIIYINTQDSRMMYFSQYFNIVALQLFYLSASINPILY
 NLISKKYRAAARLLRESRAGPSGVCGRGPEQDVAGDTGGDTAGCTETSANTKTA
 A

SEQ. ID. NO. 3

ATGGGCGGCCCCGGGAACAGCAGCGACGGCGCGGAGGGCGCGCAGCTGCCGTG
 CGACGAGCGCCTGTGCTCGCCCTTCCCCCTGGGGGCGCTGGTGCCGGTGACGGCC
 GTGTGCCTGGGCCTGTTCCGCGTCGGCGTGAGCGGCAACCTGGTGACGGTGCTGC
 TGATCGGCCGCTACCGCGACATGCGCACCACCACCAACCTGTACCTGGGCAGCA
 TGGCCGTGTCCGACCTGCTCATCCTGCTGGGGCTGCCCTCGACCTGTACCGCCT

GTGGCGCTCGCGGCCCTGGGTGTTTCGGGCAGCTGCTGTGCCGCCTGTCGCTGTAC
CTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACGTGACGGCGCTGAGCGTC
GAGCGCTACCTGGCCGTGTGCCGCCCGCTCCGCGCCCGCGCGCTGCTGTCCCGGC
GCCGCGCCCGCGCGCTCATCGCGGCGCTCTGGGCCGTGGCGCTGCTGTCGGCCGC
5 GCCCTTCTTCTTCTCTGGTGGGCGTCGAGCAGGACGCGGGCGGCCCGGCCTCAAC
GGCAGCGCGCGGCTGGCGCGGGCGCCCTCCCCGCCGCCGGGGCCCGAGGCGGCG
CTCTTCAGCCGGGAGTGCCGGCCCAGCCCGTCGCAAGCTGGGCGCGCTGCGCGTC
ATGCTCTGGGTACACCACGCCTACTTCTTCTTCCCTGCCCTTCTGTGCCTCTGCGTCCT
GTACGGGCGCATCGGCCGCGAGCTGCGGAGGCGCCGGGGGCGCTGCGGGGCC
10 GGGCCGCCTCGGGGCGCGAGCGGGGCCACCGCCAGGCCGTCCGCGTGCTG

SEQ. ID. NO. 4

ATGGGCAGCCCCTGGAACGGCAGCGACGGCCCCGAGGACGCGCGGGAGCCGCC
GTGGGCCGCGCTGCCGCCGTGCGATGAGCGCCGCTGCTCGCCCTTCCCCTTGGGC
15 ACGCTGGTGCCTGTGACGGCCGTGTGCCTGGGCCTGTTCCGCCGTCGGGGTGAGCG
GCAACGTGGTGACCGTGCTGCTGATCGGGCGCTACCGGGACATGCGGACCACCA
CCAACCTGTACCTGGGCAGCATGGCCGTGTCCGACCTGCTCATCCTGCTCGGGCT
GCCCTTCGACCTGTACCGCCTGTGGCGCTCGAGGCCCTGGGTGTTCCGACAGCTG
CTCTGCCGCCTGTGCTGTACGTGGGCGAGGGCTGCACCTACGCCTCGCTGCTGC
20 ACATGACGGCGCTCAGCGTGAGCGCTACCTGGCCATCTGCCGCCCGCTGCGTG
CCCGCGTCTTGGTCACCCGCCGCCGGGTCCGCGCGCTCATCGCCGCGCTCTGGGC
CGTGGCGCTGCTTTCGGCCGGGCCCTTCTTCTTCTGGTGGGCGTCGAGCAGGAC
CCCGCGGTCTTCGCGGCCCGGACCGCAACGGTACTGTGCCGCTGGACCCCTCGT
CGCCCGCCCCGGCGTCCCCGCCGTGGGGCCCCGGAGCGGAGGCCGCGGCTCTGT
25 TCAGCCGCGAGTGCCGGCCGAGCCGCGCGCAGCTGGGCTTGCTGCGCGTCATGC
TGTGGGTACCACCGCCTACTTTTCTTCTGCCCTTCTCTGCCTCAGCATCTCTAC
GGGCTCATCGCGCGGCAGCTGTGGCGGGGTCGGGGCCCGCTGCGAGGCCCGGCG
GCCACGGGTCGGGAGAGGGGGCCACCGGCAGACCGTCCGCGTCCTGCTGGTGGTG
GTTCTGGCCTTTATAGTGTGCTGGCTGCCTTTCCACGTTGGCAGGATCATTTACAT
30 AAACACCCAAGACTCGCGGATGATGTACTTCTCCCAGTACTTTAACATTGTCGCG
CTGCAGCTTTTCTACCTGAGTGCGTCCATCAACCCAATCCTCTACAACCTCATCTC
CAAGAAGTACAGAGCGGCTGCCCGCAGACTGCTGCGCGAAAGCCGAGCGGGGC
CCAGTGGTGTGTGCGGAAGCAGGGGCCCTGAGCAGGACGTTGCAGGGGACACTG

GCGGAGACACAGCTGGCTGCACCGAGACCAGCGCTAACACAAAGACGGCTGCAT
AG

- Other embodiments are within the following claims. While several
- 5 embodiments have been shown and described, various modifications may be made without
departing from the spirit and scope of the present invention.

WHAT IS CLAIMED IS:

1. A purified polypeptide comprising a unique amino acid region of SEQ. ID. NO. 1 or SEQ. ID. NO. 2 that is at least 9 contiguous amino acids in length, wherein said
5 unique region is not present in SEQ. ID. NO. 5 or SEQ. ID. NO. 6.

2. The polypeptide of claim 1, wherein said unique region is from SEQ. ID. NO. 1.

10 3. The polypeptide of claim 2, wherein said unique region comprises an amino acid sequence selected from the group consisting of:
GPGNSSDGA (SEQ. ID. NO. 9);
VCLGLFAVG (SEQ. ID. NO. 10);
ALLSSRRRA (SEQ. ID. NO. 11);
15 APFFFLVGVEQDAGG (SEQ. ID. NO. 12); and
CLCVLYGRI (SEQ. ID. NO. 13).

20 4. The polypeptide of claim 2, wherein said polypeptide comprises the amino acid sequence of SEQ. ID. NO. 1.

5. The polypeptide of claim 4, wherein said polypeptide consists of the amino acid sequence of SEQ. ID. NO. 1.

25 6. The polypeptide of claim 1, wherein said unique region is from SEQ. ID. NO. 2.

7. The polypeptide of claim 6, wherein said unique region comprises an amino acid sequence selected from the group consisting of:
DPAVFAAPDR (SEQ. ID. NO. 14);
30 NGTVPLDPS (SEQ. ID. NO. 15);
SPAPASPPSGPG (SEQ. ID. NO. 16);
RLLRESRAG (SEQ. ID. NO. 17); and
SGVCGSRGPEQD (SEQ. ID. NO. 18).

8. The polypeptide of claim 6, wherein said polypeptide comprises the amino acid sequence of SEQ. ID. NO. 2.

9. The polypeptide of claim 8, wherein said polypeptide consists of the amino acid sequence of SEQ. ID. NO. 2.

10. A purified nucleic acid comprising a nucleotide sequence encoding for the polypeptide of any one of claims 1-9.

11. A purified nucleic acid comprising a unique nucleotide sequence region of SEQ. ID. NO. 3 or SEQ. ID. NO. 4 that is at least 18 contiguous nucleotides in length or the complement thereof, wherein said unique region is not present in SEQ. ID. NO. 7 or SEQ. ID. NO. 8.

12. The purified nucleic acid of claim 11, wherein said unique sequence region is from SEQ. ID. NO. 3.

13. The purified nucleic acid of claim 12, wherein said unique region comprises a nucleotide sequence selected from the group consisting of:
GGCCCCGGGAACAGCAGCGACGGCGCG (SEQ. ID. NO. 19);
GGCCGTGTGCCTGGGCCT (SEQ. ID. NO. 20);
CGCGCGCTGCTGTCCCGG (SEQ. ID. NO. 21);
AGGACGCGGGCGGCCCGG (SEQ. ID. NO. 22); and
CCGCGAGCTGCGGAGGCG (SEQ. ID. NO. 23).

14. The purified nucleic acid of claim 12, wherein said nucleic acid comprises the nucleotide sequence of SEQ. ID. NO. 3.

15. The purified nucleic acid of claim 14, wherein said nucleic acid consists of the nucleotide sequence of SEQ. ID. NO. 3.

16. The purified nucleic acid of claim 11, wherein said unique sequence region is from SEQ. ID. NO. 4.

17. The purified nucleic acid of claim 16, wherein said unique region comprises a sequence selected from the group consisting of:

TTCGGCCGGGCCCTTCTTCTTT (SEQ. ID. NO. 24);

GGTCTTCGCGGCCCCGGA (SEQ. ID. NO. 25);

5 CGGTACTGTGCCGCTGGA (SEQ. ID. NO. 26);

GCTTTTCTACCTGAGTGCGTCC (SEQ. ID. NO. 27); and

CGAGCGGGGCCCAAGTGGTG (SEQ. ID. NO. 28).

18. The purified nucleic acid of claim 16, wherein said nucleic acid
10 comprises the nucleotide sequence of SEQ. ID. NO. 4.

19. The purified nucleic acid of claim 18, wherein said nucleic acid consists of the nucleotide sequence of SEQ. ID. NO. 4.

15 20. An expression vector comprising a recombinant nucleotide sequence encoding for a unique amino acid region of SEQ. ID. NO. 1 or SEQ. ID. NO. 2 that is at least 9 contiguous amino acids in length, wherein said unique region is not present in SEQ. ID. NO. 5 or SEQ. ID. NO. 6.

20 21. A recombinant cell comprising an expression vector encoding for a unique amino acid region of SEQ. ID. NO. 1 or SEQ. ID. NO. 2, that is at least 9 contiguous amino acids in length, functionally coupled to a promoter recognized by said cell, wherein said unique region is not present in SEQ. ID. NO. 5 or SEQ. ID. NO. 6.

25 22. A recombinant cell made by a process comprising the step of introducing into said cell an expression vector encoding for a unique amino acid region of SEQ. ID. NO. 1 or SEQ. ID. NO. 2, that is at least 9 contiguous amino acids in length wherein said unique region is not present in SEQ. ID. NO. 5 or 6.

30 23. A method of measuring the ability of a compound to effect motilin receptor activity comprising the steps of:

a) contacting a recombinant cell with said compound, wherein said recombinant cell comprises a recombinant nucleic acid expressing a functional motilin receptor that comprises a unique amino acid region of SEQ. ID. NO. 1 or SEQ. ID. NO. 2

that is at least 9 contiguous amino acids in length, provided that said unique region is not present in SEQ. ID. NO. 5 or 6; and

b) measuring motilin receptor activity.

- 5 24. A method of preparing a motilin receptor polypeptide comprising the step of growing the recombinant cell of claim 21 under conditions wherein said polypeptide is expressed from said expression vector.

	1		50
huMTLr	MGSPWNGSDG	PEGAREPPWP	ALPPCDERRC
dogMTLr	MGGPGNSSDG	AEGAQ.....	.LP.CDERLC
rabMTLr	MGSPWNGSDG	PEDAREPPWA	ALPPCDERRC
fish75e7	MPWTRPQVDL	HAAAAETMDQ	YTTDDHHYEG
		SLFPASTLIP	VTVICILIFV
	51		100
huMTLr	VGVSIGNVTV	MLIGRYRDMR	TTTNLYLGSM
dogMTLr	VGVSIGNLTV	LLIGRYRDMR	TTTNLYLGSM
rabMTLr	VGVSIGNVTV	MLIGRYRDMR	TTTNLYLGSM
fish75e7	VGVTGNTMTI	LIIQYFKDMK	TTTNLYLSSM
		AVSDLVIFLC	LPFDLYRLWK
	101		150
huMTLr	SRPWVFGPLL	CRLSLYVGEG	CTYATLLHMT
dogMTLr	SRPWVFGQLL	CRLSLYLGE	CTYATLLHVT
rabMTLr	SRPWVFGQLL	CRLSLYVGEG	CTYASLLHMT
fish75e7	YVPWLFGEAV	CRLYHYIFEG	CTSATILHIT
		ALSIERYLAI	SFPLRSKVMV
	151		200
huMTLr	TRRRVRALIA	VLWAVALLSA	GPFLFLVGVE
dogMTLr	SRRRARALIA	ALWAVALLSA	APFFFLVGVE
rabMTLr	TRRRVRALIA	ALWAVALLSA	GPFFFLVGVE
fish75e7	TRRRVQYIIL	ALWCFALVSA	APTLFLVGVE
		YDNET..HPD	YN.....
	201		250
huMTLr	PLASSPPLWL	SRAPPPSPPS	GPETAEEAAL
dogMTLrRAP..SPPP	GPE....AAL
rabMTLr	SPAP.ASPPS	GPG.AEEAAL
fish75e7T	GQCKHTGYAI
		SS.....	..GQLHIMTW
	251		300
huMTLr	VTTAYFFLPF	LCLSILYGLI	GRELWSSRRP
dogMTLr	VTTAYFFLPF	LCLCVLYGRI	GRELRRRRGP
rabMTLr	VTTAYFFLPF	LCLSILYGLI	ARQLWRGRGP
fish75e7	VSTTYFFCPM	LCLLFYGS	GCKLWKSND
		LQGPCALARE	RSHRQTVKIL
	301		350
huMTLr	LVVVLAFIIC	WLPFHVGRII	YINTEDSRMM
dogMTLr
rabMTLr	LVVVLAFIVC	WLPFHVGRII	YINTQDSRMM
fish75e7	VVVVLAFIIC	WLPYHIGRNL	FAQVDDYDTA
		MLSQNFNMA	MVLCYLSASI
	351		400
huMTLr	NPILYNLISK	KYRAAAFLL	LARKSRPRGF
dogMTLr
rabMTLr	NPILYNLISK	KYRAAARRLL	RESRAGPSGV
fish75e7	NPVVYNLMSR	KYRAAAKRLF	LLHQ.RPKPA
		HR.....	.GQGQFCMIG
	401	412	
huMTLr	YTETSANVKT	MG	(SEQ. ID. NO. 6)
dogMTLr	(SEQ. ID. NO. 1)
rabMTLr	CTETSANTKT	AA	(SEQ. ID. NO. 2)
fish75e7	HSPTLDESLT	GV	(SEQ. ID. NO. 5)

FIG. 1

	1		50
rabMTLr	ATGGGCAGCC CCTGGAACGG CAGCGACGGC CCCGAGGACG CGCGGGAGCC		
huMTLr	ATGGGCAGCC CCTGGAACGG CAGCGACGGC CCCGAGGGGG CGCGGGAGCC		
dogMTLr	ATGGGCGGCC CCGGGAACAG CAGCGACGGC GCGGAGGGCG CGC...AG..		
fish75e7	ATGCCCTGGA CCAG..ACCC CAGGTGGACC TCCATGCTGC TGCAGCAGAG		
	51		100
rabMTLr	GCCGTGGGCC GCGCTGCCGC CGTGCGATGA GCGCCGCT..GCTCGC		
huMTLr	GCCGTGGGCC GCGCTGCCGC CTTGCGACGA GCGCCGCT..GCTCGC		
dogMTLrC.TGC CGTGCGACGA GCGCCTGT..GCTCGC		
fish75e7	ACCATGGACC AGTA...CAC CACG.GACGA CCACCACTAC GAGGGCTCCC		
	101		150
rabMTLr	CCTTCCCCTT GGGCACGCTG GTGCCGTGTA CGGCCGTGTG CCTGGGCCTG		
huMTLr	CCTTTCCCCTT GGGGGCGCTG GTGCCGGTGA CCGCTGTGTG CCTGTGCCTG		
dogMTLr	CCTTCCCCTT GGGGGCGCTG GTGCCGGTGA CGGCCGTGTG CCTGGGCCTG		
fish75e7	TCTTCCCCGC GTCCACCCTC ATCCCCGTCA CGGTCATCTG CATCCTCATC		
	151		200
rabMTLr	TTCGCCGTCG GGGTGAGCGG CAACGTGGTG ACCGTGCTGC TGATCGGGCG		
huMTLr	TTCGTCTGTCG GGGTGAGCGG CAACGTGGTG ACCGTGATGC TGATCGGGCG		
dogMTLr	TTCGCCGTCG GCGTGAGCGG CAACCTGGTG ACGGTGCTGC TGATCGGGCG		
fish75e7	TTCGTGGTCG GCGTGACCGG CAACACCATG ACCATCCTCA TCATCCAGTA		
	201		250
rabMTLr	CTACCGGGAC ATGCGGACCA CCACCAACCT GTACCTGGGC AGCATGGCCG		
huMTLr	CTACCGGGAC ATGCGGACCA CCACCAACTT GTACCTGGGC AGCATGGCCG		
dogMTLr	CTACCGCGAC ATGCGCACCA CCACCAACCT GTACCTGGGC AGCATGGCCG		
fish75e7	CTTCAAGGAC ATGAAGACCA CCACCAACCT GTACCTGTCC AGCATGGCCG		
	251		300
rabMTLr	TGTCCGACCT GCTCATCTG CTCGGGCTGC CTTTCGACCT GTACCGCCTG		
huMTLr	TGTCCGACCT ACTCATCTG CTCGGGCTGC CGTTCGACCT GTACCGCCTC		
dogMTLr	TGTCCGACCT GCTCATCTG CTGGGGCTGC CCCTCGACCT GTACCGCCTG		
fish75e7	TGTCCGACCT CGTCATCTT CTCTGCCTGC CTTTCGACCT GTACCGCCTG		
	301		350
rabMTLr	TGGCGCTCGA GGCCCTGGGT GTTCGGACAG CTGCTCTGCC GCCTGTCTGCT		
huMTLr	TGGCGCTCGC GGCCCTGGGT GTTCGGGCCG CTGCTCTGCC GCCTGTCTGCT		
dogMTLr	TGGCGCTCGC GGCCCTGGGT GTTCGGGCAG CTGCTGTGCC GCCTGTCTGCT		
fish75e7	TGGAAGTACG TGCCGTGGCT GTTCGGCGAG GCCGTGTGCC GCCTCTACCA		
	351		400
rabMTLr	GTACGTGGGC GAGGGCTGCA CCTACGCCTC GCTGCTGCAC ATGACGGCGC		
huMTLr	CTACGTGGGC GAGGGCTGCA CCTACGCCAC GCTGCTGCAC ATGACGGCGC		
dogMTLr	GTACCTGGGC GAGGGCTGCA CCTACGCCAC GCTGCTGCAC GTGACGGCGC		
fish75e7	CTACATCTTC GAAGGCTGCA CGTCGGCCAC CATCTCCAC ATCACGGCCC		
	401		450
rabMTLr	TCAGCGTGGA GCGCTACCTG GCCATCTGCC GCCCGCTGCG TGCCCGCGTC		
huMTLr	TCAGCGTCGA GCGCTACCTG GCCATCTGCC GCCCGCTCCG CGCCCGCGTC		
dogMTLr	TGAGCGTCGA GCGCTACCTG GCCGTGTGCC GCCCGCTCCG CGCCCGCGCG		
fish75e7	TGAGCATCGA GCGCTACCTG GCCATCAGCT TCCCCCTCAG GAGCAAGGTG		

FIG. 2A

	451		500
rabMTLr	TTGGTCACCC	GCCGCCGGGT	CCGCGCGCTC ATCGCCGCGC TCTGGGCCGT
huMTLr	TTGGTCACCC	GGCGCCGCGT	CCGCGCGCTC ATCGCTGTGC TCTGGGCCGT
dogMTLr	CTGCTGTCCC	GGCGCCGCGC	CCGCGCGCTC ATCGCGGCGC TCTGGGCCGT
fish75e7	ATGGTGACCA	GGAGAAAGGT	CCAGTACATC ATCCTGGCCC TGTGGTGCTT
	501		550
rabMTLr	GGCGCTGCTT	TCGGCCGGGC	CCTTCTTCTT TCTGGTGGGC GTCGAGCAGG
huMTLr	GGCGCTGCTC	TCTGCCGGTC	CCTTCTTGTT CCTGGTGGGC GTCGAGCAGG
dogMTLr	GGCGCTGCTG	TCGGCCGCGC	CCTTCTTCTT CCTGGTGGGC GTCGAGCAGG
fish75e7	CGCCCTGGTG	TCGGCCGCTC	CCACGCTCTT CCTGGTCGGG GTGGAGTACG
	551		600
rabMTLr	ACCCCGCGGT	CTTCGCGGCC	CCGGACCGCA ACGGTACTGT GCCGCTGGAC
huMTLr	ACCCCGGCAT	CTCCGTAGTC	CCGGGCCTCA ATGGCACCGC GCCGATCGCC
dogMTLr	ACGCGG....GCGGCC	CCGG.CCTCA ACGGCAGCGC GCCGCTGG..
fish75e7	ACAACG....AGAC	GCA..CCCCG ACTACAACAC G.GG.....
	601		650
rabMTLr	CCCTCGTCGC	CCGCC.....CC
huMTLr	TCCTCGCCTC	TCGCCTCGTC	GCCGCCTCTC TGGCTCTCGC GGGCGCCACC
dogMTLrC	GCGGG.....C
fish75e7
	651		700
rabMTLr	GGCGTCCCCG	CCGTCCGGGC	CCGGA...GC GGAGGCCGCG GCTCTGTTCA
huMTLr	GCCGTCCCCG	CCGTCCGGGC	CCGAGACCGC GGAGGCCGCG GCGCTGTTCA
dogMTLr	GCCCTCCCCG	CCGCCGGGGC	CCGAG.....G...CG GCGCTCTTCA
fish75e7C	CAGTG.....
	701		750
rabMTLr	GCCGCGAGTG	CCGGCCGAGC	CGCGCGCAGC TGGGCTT.GC TGCGCGTCAT
huMTLr	GCCGCGAATG	CCGGCCGAGC	CCCGCGCAGC TGGGCGC.GC TGCGTGTCAT
dogMTLr	GCCGGGAGTG	CCGGCCCAGC	CCGTCGCAGC TGGGCGC.GC TGCGCGTCAT
fish75e7	..CAAGCACA	CGGGCTACGC	CAT...CAGC TCGGGGCAGC TGCACATCAT
	751		800
rabMTLr	GCTGTGGGTT	ACCACCGCCT	ACTTTTTCCT GCCCTTCCTC TGCCTCAGCA
huMTLr	GCTGTGGGTC	ACCACCGCCT	ACTTCTTCCT GCCCTTTCTG TGCCTCAGCA
dogMTLr	GCTCTGGGTC	ACCACCGCCT	ACTTCTTCCT GCCCTTCCTG TGCCTCTGCG
fish75e7	GATCTGGGTG	TCCACCACCT	ACTTCTTCTG CCCGATGCTG TGTCTCCTCT
	801		850
rabMTLr	TCCTCTACGG	GCTCATCGCG	CGGCAGCTGT GGCGGGGTCG GGGCCCGCTG
huMTLr	TCCTCTACGG	GCTCATCGGG	CGGGAGCTGT GGAGCAGCCG GCGGCCGCTG
dogMTLr	TCCTGTACGG	GCGCATCGGC	CGCGAGCTGC GGAGGCGCCG GGGGCCGCTG
fish75e7	TCCTCTACGG	CTCCATCGGG	TGCAAGCTGT GGAAGAGCAA GAACGACCTG

FIG. 2B

	851		900
rabMTLr	CGAGGCCCGG CGGCCACGGG TCGGGAGAGG GGCCACCGGC AGACCGTCCG		
huMTLr	CGAGGCCCGG CCGCCTCGGG GCGGGAGAGA GGCCACCGGC AGACCGTCCG		
dogMTLr	CGGGGCCGGG CCGCCTCGGG GCGCGAGCGG GGCCACCGCC AGGCCGTCCG		
fish75e7	CAGGGCCCGT GCGCCCTGGC CCGCGAGAGG TCGCACAGGC AAACGGTGAA		
	901		950
rabMTLr	CGTCCTGCTG GTGGTGGTTC TGGCCTTTAT AGTGTGCTGG CTGCCCTTTC		
huMTLr	CGTCCTGCTG GTGGTGGTTC TGGCATTAT AATTGCTGG TTGCCCTTTC		
dogMTLr	CGTGCTG... ..		
fish75e7	GATCCTGGTG GTGGTGGTGC TGGCCTTCAT CATCTGCTGG CTGCCCTACC		
	951		1000
rabMTLr	ACGTTGGCAG GATCATTTAC ATAAACACCC AAGACTCGCG GATGATGTAC		
huMTLr	ACGTTGGCAG AATCATTTAC ATAAACACGG AAGATTCGCG GATGATGTAC		
dogMTLr		
fish75e7	ACATCGGCAG GAACCTGTTC GCCCAGGTGG ACGACTACGA CACGGCCATG		
	1001		1050
rabMTLr	TTCTCCAGT ACTTTAACAT TGTCGCGCTG CAGCTTTTCT ACCTGAGTGC		
huMTLr	TTCTCTCAGT ACTTTAACAT CGTCGCTCTG CAACTTTTCT ATCTGAGCGC		
dogMTLr		
fish75e7	CTCAGCCAGA ATTTCAACAT GGCCTCCATG GTGCTCTGCT ACCTCAGCGC		
	1051		1100
rabMTLr	GTCCATCAAC CCAATCCTCT ACAACCTCAT CTCCAAGAAG TACAGAGCGG		
huMTLr	ATCTATCAAC CCAATCCTCT ACAACCTCAT TTCAAAGAAG TACAGAGCGG		
dogMTLr		
fish75e7	CTCCATCAAC CCCGTCGTCT ACAACCTGAT GTCGAGGAAG TACCGGGCCG		
	1101		1150
rabMTLr	CTGCC...CG CAGACTGCTG CGCGAAAGCC GAGCGGGGCC CAGTGGTGTG		
huMTLr	CGGCC...TT TAAACTGCTG CTCGCAAGGA AGTCCAGGCC GAGAGGCTTC		
dogMTLr		
fish75e7	CCGCCAAGCG CCTCTTCCTG CTCCACCAGA GACCCAAGCC ..GGCCCACC		
	1151		1200
rabMTLr	TGCGGAAGCA GGGGCCCTGA GCAGGACGTT GCAGGGG.AC ACTGGCGGAG		
huMTLr	CACAGAAGCA GGGACACTGC GGGGGAAGTT GCAGGGG.AC ACTGGAGGAG		
dogMTLr		
fish75e7	GGGGGCAGGG GCAGTTTTCG ATGATCGGCC ACAGCCCCAC CCTGGACGAG		
	1201		1250
rabMTLr	ACACAGCTGG CTGCACCGAG ACCAGCGCTA ACACAAAGAC GGCTGCATAG		
huMTLr	ACACGGTGGG CTACACCGAG ACAAGCGCTA ACGTGAAGAC GATGGGATAA		
dogMTLr		
fish75e7	AGCCTGACGG GGGTGTGA.. ..		
rabMTLr	(SEQ. ID. NO. 4)		
huMTLr	(SEQ. ID. NO. 7)		
dogMTLr	(SEQ. ID. NO. 3)		
fish75e7	(SEQ. ID. NO. 8)		

FIG. 2C

SEQUENCE LISTING

<110> Merck & Co., Inc.

<120> DOG AND RABBIT MOTILIN RECEPTOR
ORTHOLOGS

<130> PCT 20390

<150> 60/162,264

<151> 1999-10-29

<160> 32

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 271

<212> PRT

<213> Dog

<400> 1

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      20          25          30
Pro Val Thr Ala Val Cys Leu Gly Leu Phe Ala Val Gly Val Ser Gly
      35          40          45
Asn Leu Val Thr Val Leu Leu Ile Gly Arg Tyr Arg Asp Met Arg Thr
 50          55          60
Thr Thr Asn Leu Tyr Leu Gly Ser Met Ala Val Ser Asp Leu Leu Ile
65          70          75          80
Leu Leu Gly Leu Pro Leu Asp Leu Tyr Arg Leu Trp Arg Ser Arg Pro
      85          90          95
Trp Val Phe Gly Gln Leu Leu Cys Arg Leu Ser Leu Tyr Leu Gly Glu
      100          105          110
Gly Cys Thr Tyr Ala Thr Leu Leu His Val Thr Ala Leu Ser Val Glu
      115          120          125
Arg Tyr Leu Ala Val Cys Arg Pro Leu Arg Ala Arg Ala Leu Leu Ser
      130          135          140
Arg Arg Arg Ala Arg Ala Leu Ile Ala Ala Leu Trp Ala Val Ala Leu
145          150          155          160
Leu Ser Ala Ala Pro Phe Phe Phe Leu Val Gly Val Glu Gln Asp Ala
      165          170          175
Gly Gly Pro Gly Leu Asn Gly Ser Ala Arg Leu Ala Arg Ala Pro Ser
      180          185          190
Pro Pro Pro Gly Pro Glu Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro
      195          200          205
Ser Pro Ser Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr
      210          215          220
Ala Tyr Phe Phe Leu Pro Phe Leu Cys Leu Cys Val Leu Tyr Gly Arg
225          230          235          240
Ile Gly Arg Glu Leu Arg Arg Arg Arg Gly Pro Leu Arg Gly Arg Ala
      245          250          255
Ala Ser Gly Arg Glu Arg Gly His Arg Gln Ala Val Arg Val Leu
      260          265          270

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<210> 2

<211> 400

<212> PRT

<213> Rabbit

<400> 2

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 20          25          30
Phe Pro Leu Gly Thr Leu Val Pro Val Thr Ala Val Cys Leu Gly Leu
 35          40          45
Phe Ala Val Gly Val Ser Gly Asn Val Val Thr Val Leu Leu Ile Gly
 50          55          60
Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met
 65          70          75          80
Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr
 85          90          95
Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Gln Leu Leu Cys Arg
100          105          110
Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Ser Leu Leu His
115          120          125
Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu
130          135          140
Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala
145          150          155          160
Ala Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Phe Phe Leu
165          170          175
Val Gly Val Glu Gln Asp Pro Ala Val Phe Ala Ala Pro Asp Arg Asn
180          185          190
Gly Thr Val Pro Leu Asp Pro Ser Ser Pro Ala Pro Ala Ser Pro Pro
195          200          205
Ser Gly Pro Gly Ala Glu Ala Ala Leu Phe Ser Arg Glu Cys Arg
210          215          220
Pro Ser Arg Ala Gln Leu Gly Leu Leu Arg Val Met Leu Trp Val Thr
225          230          235          240
Thr Ala Tyr Phe Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly
245          250          255
Leu Ile Ala Arg Gln Leu Trp Arg Gly Arg Gly Pro Leu Arg Gly Pro
260          265          270
Ala Ala Thr Gly Arg Glu Arg Gly His Arg Gln Thr Val Arg Val Leu
275          280          285
Leu Val Val Val Leu Ala Phe Ile Val Cys Trp Leu Pro Phe His Val
290          295          300
Gly Arg Ile Ile Tyr Ile Asn Thr Gln Asp Ser Arg Met Met Tyr Phe
305          310          315          320
Ser Gln Tyr Phe Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala
325          330          335
Ser Ile Asn Pro Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala
340          345          350
Ala Ala Arg Arg Leu Leu Arg Glu Ser Arg Ala Gly Pro Ser Gly Val
355          360          365
Cys Gly Ser Arg Gly Pro Glu Gln Asp Val Ala Gly Asp Thr Gly Gly
370          375          380
Asp Thr Ala Gly Cys Thr Glu Thr Ser Ala Asn Thr Lys Thr Ala Ala
385          390          395          400

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<210> 3

<211> 813

<212> DNA

<213> Dog

<400> 3

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ctgttcgccg tcggcgtgag cggcaacctg gtgacgggtgc tgctgatcgg ccgctaccgc      180
gacatgcgca ccaccacaa cctgtacctg ggcagcatgg ccgtgtccga cctgtctcat      240

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ctgctggggc	tgccccctga	cctgtaccgc	ctgtggcgct	cgcgccctg	ggtgttcggg	300
cagctgctgt	gccgcctgtc	gctgtacctg	ggcgagggct	gcacctacgc	cacgctgctg	360
cacgtgacgg	cgctgagcgt	cgagcgctac	ctggccgtgt	gccgcccgt	ccgcgccccg	420
gcgctgctgt	cccggcgccg	cgcccgcgcg	ctcatcgcg	cgctctgggc	cgtggcgctg	480
ctgtcgggcg	cgcccttctt	cttcctgggt	ggcgctcgag	aggacgcggg	cgcccccggc	540
ctcaacggca	gcgcgcggct	ggcgcgggcg	ccctccccgc	cgccggggcc	cgaggcgggc	600
ctcttcagcc	gggagtgcgg	gcccagcccc	tcgcagctgg	gcgcgctgcg	cgtcatgctc	660
tgggtcacca	ccgcctactt	cttcctgccc	ttcctgtgcc	tctgcgtcct	gtacggggcg	720
atcgggcgcg	agctgcggag	gcgcgggggg	ccgctgcggg	gccggggccg	ctcggggcg	780
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 <211> 1203
 <212> DNA
 <213> Rabbit

<400> 4						
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gtgacggccg	tgtgcctggg	cctgttcgcc	gtcggggtga	gcggcaacgt	ggtgaccgtg	180
ctgctgatcg	ggcgctaccg	ggacatgcgg	accaccacca	acctgtacct	gggcagcatg	240
gccgtgtccg	acctgctcat	cctgctcggg	ctgcccttcg	acctgtaccg	cctgtggcgc	300
tcgagggcct	gggtgttcgg	acagctgctc	tgccgcctgt	cgctgtacgt	gggcgagggc	360
tgcacctacg	cctcgctgct	gcacatgacg	gcgctcagcg	tggagcgcta	cctggccatc	420
tgccgcccgc	tgcgtgcccg	cgtcttggtc	accgcgcgcc	gggtccgcgc	gctcatcgcc	480
gcgctctggg	ccgtggcgct	gctttcggcc	gggcccttct	tctttctggt	gggcgtcgag	540
caggaccccc	cggtcttcgc	ggccccggac	cgcaacggta	ctgtgccgct	ggaccctcgc	600
tcgcccggcc	cggcgtcccc	gccgtcgggg	cccgagcgcg	aggccgcggc	tctgttcagc	660
cgcgagtgcc	ggccgagccg	cgcgcgctg	ggcttgctgc	gcgtcatgct	gtgggttacc	720
accgcctact	tttctctgcc	cttcctctgc	ctcagcatcc	tctacgggct	catcgcgcg	780
cagctgtggc	ggggtcgggg	cccgtcgca	ggcccggcgg	ccacgggtcg	ggagaggggc	840
caccggcaga	ccgtccgcgt	cctgctgggt	gtggttcttg	cctttatagt	gtgctggctg	900
cctttccacg	ttggcaggat	catttacata	aacacccaag	actcgcggat	gatgtacttc	960
tcccagttact	ttaacattgt	cgcgctgcag	cttttctacc	tgagtgcgtc	catcaacca	1020
atcctctaca	acctcatctc	caagaagtac	agagcggctg	cccgcagact	gctgcgcgaa	1080
agccgagcgg	ggcccagtg	tgtgtgcgga	agcagggggc	ctgagcagga	cgttgccagg	1140
gacactggcg	gagacacagc	tggctgcacc	gagaccagcg	ctaacacaaa	gacggctgca	1200
tag						1203

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 <212> PRT
 <213> Human

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35 40 45	
Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly	
50 55 60	
Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met	
65 70 75 80	
Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr	
85 90 95	
Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg	
100 105 110	
Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His	
115 120 125	

Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu
 130 135 140
 Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala
 145 150 155 160
 Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu
 165 170 175
 Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn
 180 185 190
 Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu
 195 200 205
 Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr
 210 215 220
 Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala
 225 230 235 240
 Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe
 245 250 255
 Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg
 260 265 270
 Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly
 275 280 285
 Arg Glu Arg Gly His Arg Gln Thr Val Arg Val Leu Leu Val Val Val
 290 295 300
 Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile
 305 310 315 320
 Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe
 325 330 335
 Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro
 340 345 350
 Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Phe Lys
 355 360 365
 Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg
 370 375 380
 Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly
 385 390 395 400
 Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly
 405 410

<210> 6
 <211> 363
 <212> PRT
 <213> Spheroides Nephelus

<400> 6
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 Thr Met Asp Gln Tyr Thr Thr Asp Asp His His Tyr Glu Gly Ser Leu
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 Phe Pro Ala Ser Thr Leu Ile Pro Val Thr Val Ile Cys Ile Leu Ile
 35 40 45
 Phe Val Val Gly Val Thr Gly Asn Thr Met Thr Ile Leu Ile Ile Gln
 50 55 60
 Tyr Phe Lys Asp Met Lys Thr Thr Thr Asn Leu Tyr Leu Ser Ser Met
 65 70 75 80
 Ala Val Ser Asp Leu Val Ile Phe Leu Cys Leu Pro Phe Asp Leu Tyr
 85 90 95
 Arg Leu Trp Lys Tyr Val Pro Trp Leu Phe Gly Glu Ala Val Cys Arg
 100 105 110
 Leu Tyr His Tyr Ile Phe Glu Gly Cys Thr Ser Ala Thr Ile Leu His
 115 120 125
 Ile Thr Ala Leu Ser Ile Glu Arg Tyr Leu Ala Ile Ser Phe Pro Leu
 130 135 140

Arg Ser Lys Val Met Val Thr Arg Arg Arg Val Gln Tyr Ile Ile Leu
 145 150 155 160
 Ala Leu Trp Cys Phe Ala Leu Val Ser Ala Ala Pro Thr Leu Phe Leu
 165 170 175
 Val Gly Val Glu Tyr Asp Asn Glu Thr His Pro Asp Tyr Asn Thr Gly
 180 185 190
 Gln Cys Lys His Thr Gly Tyr Ala Ile Ser Ser Gly Gln Leu His Ile
 195 200 205
 Met Ile Trp Val Ser Thr Thr Tyr Phe Phe Cys Pro Met Leu Cys Leu
 210 215 220
 Leu Phe Leu Tyr Gly Ser Ile Gly Cys Lys Leu Trp Lys Ser Lys Asn
 225 230 235 240
 Asp Leu Gln Gly Pro Cys Ala Leu Ala Arg Glu Arg Ser His Arg Gln
 245 250 255
 Thr Val Lys Ile Leu Val Val Val Val Leu Ala Phe Ile Ile Cys Trp
 260 265 270
 Leu Pro Tyr His Ile Gly Arg Asn Leu Phe Ala Gln Val Asp Asp Tyr
 275 280 285
 Asp Thr Ala Met Leu Ser Gln Asn Phe Asn Met Ala Ser Met Val Leu
 290 295 300
 Cys Tyr Leu Ser Ala Ser Ile Asn Pro Val Val Tyr Asn Leu Met Ser
 305 310 315 320
 Arg Lys Tyr Arg Ala Ala Ala Lys Arg Leu Phe Leu Leu His Gln Arg
 325 330 335
 Pro Lys Pro Ala His Arg Gly Gln Gly Gln Phe Cys Met Ile Gly His
 340 345 350
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 355 360

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<211> 1239

<212> DNA

<213> Human

<400> 7

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gtgaccgctg	tgtgcctgtg	cctgttcgtc	gtcggggtga	gcggcaacgt	ggtgaccgtg	180
atgctgatcg	ggcgctaccg	ggacatgcgg	accaccacca	acttgtagct	gggcagcatg	240
gccgtgtccg	acctactcat	cctgctcggg	ctgccgttcg	acctgtaccg	cctctggcgc	300
tcgcggccct	gggtgttcgg	gccgctgctc	tgccgcctgt	ccctctacgt	gggcgagggc	360
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cctctcgcct	cgtcgcgcgc	tctctggctc	tcgcgggcgc	caccgcgcgc	cccgcgcgtc	660
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tacataaaca	cggaagattc	gcggatgatg	tacttctctc	agtactttaa	catcgctcgt	1020
ctgcaacttt	tctatctgag	cgcattctatc	aacccaatcc	tctacaacct	catttcaaag	1080
aagtacagag	cggcggcctt	taaactgctg	ctcgcaagga	agtccaggcc	gagaggcttc	1140
cacagaagca	gggacactgc	gggggaagtt	gcagggggaca	ctggaggaga	cacggtgggc	1200
tacaccgaga	caagcgctaa	cgtgaagacg	atggggataa			1239

<210> 8

<211> 1092

<212> DNA

<213> Spheroides Nephelus

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gtcacggtca tctgcatcct catcttcgtg gtcggcgatga ccggcaacac catgaccatc      180
ctcatcatcc agtacttcaa ggacatgaag accaccacca acctgtacct gtccagcatg      240
gccgtgtccg acctcgctcat cttcctctgc ctgcccttcg acctgtaccg cctgtggaag      300
tacgtgccgt ggctgttcgg cgaggccgtg tgccgcctct accactacat cttcgaaggc      360
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gccctgtggt gcttcgccct ggtgtcggcc gctcccacgc tcttcctggt cggggtggag      540
tacgacaacg agacgcaccc cgactacaac acgggccagt gcaagcacac gggctacgcc      600
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atgctgtgtc tctcttccct ctacggctcc atcgggtgca agctgtggaa gagcaagaac      720
gacctgcagg gcccggtcgc cctggcccgc gagaggtcgc acaggcaaac ggtgaagatc      780
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ctgttcgccc aggtggacga ctacgacacg gccatgctca gccagaattt caacatggcc      900
tccatggtgc tctgtacct cagcgccctc atcaaccccg tcgtctacaa cctgatgtcg      960
aggaagtacc gggccgcgcg caagcgctc ttcctgctcc accagagacc caagccggcc     1020
caccgggggc aggggcagtt ttgcatgatc ggccacagcc ccaaccctgga cgagagcctg     1080
acgggggtgt ga                                     1092

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<210> 9
<211> 9
<212> PRT
<213> Dog

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 1               5

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<210> 10
<211> 10
<212> PRT
<213> Dog

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<400> 10
Val Cys Leu Gly Leu Phe Ala Val Gly Val
 1               5               10

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```

<210> 11
<211> 9
<212> PRT
<213> Dog

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<400> 11
Ala Leu Leu Ser Ser Arg Arg Arg Ala
 1               5

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<210> 12
<211> 15
<212> PRT
<213> Dog

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<400> 12
Ala Pro Phe Phe Phe Leu Val Gly Val Glu Gln Asp Ala Gly Gly
 1               5               10               15

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<210> 13
<211> 9
<212> PRT
<213> Dog

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<400> 13
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1 5

<210> 14
<211> 10
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<213> Rabbit

<400> 14
Asp Pro Ala Val Phe Ala Ala Pro Asp Arg
1 5 10

<210> 15
<211> 9
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<213> Rabbit

<400> 15
Asn Gly Thr Val Pro Leu Asp Pro Ser
1 5

<210> 16
<211> 12
<212> PRT
<213> Rabbit

<400> 16
Ser Pro Ala Pro Ala Ser Pro Pro Ser Gly Pro Gly
1 5 10

<210> 17
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<213> Rabbit

<400> 17
Arg Arg Leu Leu Arg Glu Ser Arg Ala Gly
1 5 10

<210> 18
<211> 12
<212> PRT
<213> Rabbit

<400> 18
Ser Gly Val Cys Gly Ser Arg Gly Pro Glu Gln Asp
1 5 10

<210> 19
<211> 27
<212> DNA
<213> Dog

<400> 19
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<210> 20
<211> 18
<212> DNA
<213> Dog

<400> 20
ggccgtgtgc ctgggcct 18

<210> 21
<211> 18
<212> DNA
<213> Dog

<400> 21
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<210> 22
<211> 18
<212> DNA
<213> Dog

<400> 22
aggacgcggg cggccccg 18

<210> 23
<211> 18
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<213> Dog

<400> 23
ccgcgagctg cggaggcg 18

<210> 24
<211> 22
<212> DNA
<213> Rabbit

<400> 24
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<210> 25
<211> 18
<212> DNA
<213> Rabbit

<400> 25
ggtcttcgcg gccccgga 18

<210> 26
<211> 18
<212> DNA
<213> Rabbit

<400> 26
cgggtactgtg ccgctgga 18

<210> 27
<211> 22
<212> DNA
<213> Rabbit

<400> 27
gcttttctac ctgagtgcg cc 22

<210> 28
<211> 19
<212> DNA

<213> Rabbit

<400> 28
cgagcggggc ccagtgggtg 19

<210> 29
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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<210> 31
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<220>
<223> PCR Primer

<400> 31
gtccgcgtcc tgctggtggt ggttctggcc tttatagtg 39

<210> 32
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
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<400> 32
agtttagcgg ccgcctatgc agccgtcttt gtgttagc 38

INTERNATIONAL SEARCH REPORT

 International application No.
 PCT/US00/29426

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07K 14/72; C07H 21/04; C12N 15/00, 63, 85, 86; G01N 33/53

US CL : 530/300; 536/23.5; 435/7.1, 69.1, 320.1, 325

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/300; 536/23.5; 435/7.1, 69.1, 320.1, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE

search terms: motilin receptor

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MAHAIRAS et al. Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome. Proc. Natl. Acad. Sci. USA, August 1999, Vol. 96, pages 9739-9744, see the abstract.	10
X	Nucleotide Database on PubMed, US National Library of Medicine, Bethesda, MD, USA), Accession No. AQ302307, MAHAIRAS et al. 'Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome', 16 December 1998, see the complement of nucleotides 41 to 67.	10



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*&* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

03 JANUARY 2001

Date of mailing of the international search report

08 FEB 2001

 Name and mailing address of the ISA/US
 Commissioner of Patents and Trademarks
 Box PCT
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/29426

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ZAHRAOUI et al. Nucleotide sequence of the chicken proto-oncogene c-erbA corresponding to domain 1 of v-erbA. Eur. J. Biochem. 1987, Vol. 166, pages 63-69, see the complement of nucleotides 705-725 of the sequence in Figure 2B.	11, 12
A	WO 99/64436 A1 (MERCK & CO., INC.) 16 December 1999 (16.12.99), Claim 3, Figure 3.	1-5, 10-15, 20-24

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/29426**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-5, 10-15, 20-24

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-5, 10-15, 20-24, to the extent that they are drawn to or encompass a polypeptide comprising and a polynucleotide encoding SEQ ID NO: 1.

Group II, claim(s) 1, 6-11, 16-24, to the extent that they are drawn to a polypeptide comprising and a polynucleotide encoding SEQ ID NO: 2.

The inventions listed as Groups I-II do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the special technical feature of group I is a rabbit motilin receptor. The special technical feature of group II is a dog motilin receptor. Each of the special technical features is a structurally and functionally different chemical compound each of which can be made and used without the other. Lack of unity is shown because these compounds lack a common utility which is based upon a common structural feature which has been identified as the basis for that common utility.